

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:25:20 ; Search time 32 Seconds
(without alignments)
327.502 Million cell updates/sec

Title: US-09-869-566-5

Perfect score: 1059

Sequence: 1 MSALLILALVGRAVADYKDP.....IEFSPQVCKAEMSPSEVSD 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCUTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	895	84.5	218	4	US-09-293-625-2
2	895	84.5	218	4	US-09-398-412B-4
3	863.5	81.5	218	4	US-09-398-412B-2
4	702	86.3	167	3	US-09-128-155-7
5	702	66.3	178	3	US-09-128-155-2
6	695	65.6	136	3	US-09-128-155-11
7	623	58.8	115	3	US-09-128-155-5
8	623	58.8	115	3	US-09-128-155-9
9	623	58.8	115	3	US-09-128-155-13
10	473.5	44.7	185	3	US-09-128-155-18
11	229.5	21.7	169	2	US-09-790-032-2
12	229.5	21.7	169	3	US-09-069-619-2
13	229.5	21.7	169	4	US-09-494-018-2
14	229.5	21.7	169	4	US-09-398-412B-15
15	191.5	18.1	156	4	US-09-398-412B-13
16	174.5	16.5	155	3	US-09-417-455-5
17	174.5	16.5	155	4	US-09-348-942-5
18	174.5	16.5	155	4	US-09-316-081-5
19	174.5	16.5	155	4	US-09-578-458-5
20	174.5	16.5	155	4	US-09-522-964A-5
21	174.5	16.5	155	4	US-09-457-626-5
22	174.5	16.5	155	4	US-09-576-008-5
23	171	16.1	160	4	US-09-398-412B-14
24	167	15.8	178	3	US-09-000-630C-21
25	167	15.8	178	3	US-08-862-730C-21
26	167	15.8	178	3	US-09-417-455-9
27	167	15.8	178	4	US-09-348-942-9

Sequence 9, Appli
Sequence 9, Appli
Sequence 18, Appli
Sequence 13, Appli
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178 4 US-09-457-626-9
178 4 US-09-576-008-9
152 4 US-09-578-458-18
180 1 US-08-476-860-13
180 2 US-08-910-733-13
180 2 US-08-910-884-13
159 1 US-08-459-811-2
159 2 US-08-484-598-2
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159 2 US-08-425-232-2
159 2 US-08-471-227-3
159 2 US-08-479-140-2
159 3 US-08-477-143-2
159 3 US-09-417-455-14
159 4 US-09-348-942-14
159 4 US-09-316-081-9
159 4 US-09-578-458-9

ALIGNMENTS

RESULT 1

US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; APPLICANT: McDonnell, Peter C
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293,625
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-625-2

Query Match 84.5%; Score 995; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.4e-97;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	35	PKVKNLNPKTSIHDDHKVLVDSGNLIAVPDKNIRPEIFFALASSLSASAEKGSPI	94
Db	50	PKVKNLNPKTSIHDDHKVLVDSGNLIAVPDKNIRPEIFFALASSLSASAEKGSPI	109
QY	95	LLGVSKGEFCLYCDKQKQSHPSLQKXKELMCLAAQKESARRPFI FYRAQVGSNNMLES	154
Db	110	LLGVSKGEFCLYCDKQKQSHPSLQKXKELMCLAAQKESARRPFI FYRAQVGSNNMLES	169
QY	155	AAHPGWFICTSCNCPNVGVTDKFNKRGHIEFSPQVCKAEMSPSEVSD	203
Db	170	AAHPGWFICTSCNCPNVGVTDKFNKRGHIEFSPQVCKAEMSPSEVSD	218

RESULT 2

US-09-398-412B-4
; Sequence 4, Application US/09398412B
; Patent No. 6690380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reagi
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-398-412B-4

Query Match      84.5%; Score 895; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 9.4e-97;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVKNLNPKKFSIHDDHVKVLDLSDGNLIAVPDKNIRPIFFALASSLSASAEGSPI 94
DB 50 PKVKNLNPKKFSIHDDHVKVLDLSDGNLIAVPDKNIRPIFFALASSLSASAEGSPI 109
QY 95 LLGVSKGEFLCYCDKDKGSHPSLQKKKLMKLAQKESARRPFIYEAQVGSNNMLES 154
DB 110 LLGVSKGEFLCYCDKDKGSHPSLQKKKLMKLAQKESARRPFIYEAQVGSNNMLES 169
QY 155 AAHPGWFICTSCNCPNPFVGTDFENRKHIEFSFQPVCKAEMSPSEVSD 203
DB 170 AAHPGWFICTSCNCPNPFVGTDFENRKHIEFSFQPVCKAEMSPSEVSD 218

RESULT 3
US-09-398-412B-2
; Sequence 2, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
; FILE OF INVENTION: Methods
; FILE REFERENCE: PX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-398-412B-2

Query Match      81.5%; Score 863.5; DB 4; Length 218;
Best Local Similarity 84.7%; Pred. No. 4.7e-93;
Matches 172; Conservative 5; Mismatches 11; Indels 15; Gaps 2;

QY 16 DYKDDDDKLA--AANSALCRGP-----XVKNLNPKKFSIHDDHVKVLDLSDG 60
DB 16 DWKDEPQCCLEDPAGSPLEPGPSLPTMNFVHTSRKVKSLNPKKFSIHDDHVKVLDLSDG 75
QY 61 NLIAVPDKNIRPIFFALASSLSASAEGSPIILLGVSKGEFLCYCDKDKGSHPSLQJ 120
DB 76 NLIAVPDKNIRPIFFALASSLSASAEGSKILLGVSKGEFLCYCDKDKGSHPSLQJ 135
QY 121 KKEKLMKLAQKESARRPFIYEAQVGSNNMLESAAHPGWFICTSCNCPNPFVGTDFEN 180
DB 136 KKEKLMKLAQKESARRPFIYEAQVGSNNMLESAAHPGWFICTSCNCPNPFVGTDFEN 195
QY 181 RKHIEFSFQPVCKAEMSPSEVSD 203
DB 196 RKHIEFSFQPVCKAEMSPSEVSD 218

RESULT 4
US-09-128-155-7
; Sequence 7, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Fan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
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; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-7

Query Match      66.3%; Score 702; DB 3; Length 167;
Best Local Similarity 93.6%; Pred. No. 2.8e-74;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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DB 28 SLPTMNFVHTKIRFFALASSLSASAEGSPIILLGVSKGEFLCYCDKDKGSHPSLQKKE 87
QY 124 KLMKLAQKESARRPFIYEAQVGSNNMLESAAHPGWFICTSCNCPNPFVGTDFENRKH 183
DB 88 KLMKLAQKESARRPFIYEAQVGSNNMLESAAHPGWFICTSCNCPNPFVGTDFENRKH 147
QY 184 IEFSFQPVCKAEMSPSEVSD 203
DB 148 IEFSFQPVCKAEMSPSEVSD 167

RESULT 5
US-09-128-155-2
; Sequence 2, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Fan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-2

Query Match      66.3%; Score 702; DB 3; Length 178;
Best Local Similarity 93.6%; Pred. No. 3.1e-74;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 64 AVPDKNYIRPIFFALASSLSASAEGSPIILLGVSKGEFLCYCDKDKGSHPSLQKKE 123
DB 39 SLPTMNFVHTKIRFFALASSLSASAEGSPIILLGVSKGEFLCYCDKDKGSHPSLQKKE 98
QY 124 KLMKLAQKESARRPFIYEAQVGSNNMLESAAHPGWFICTSCNCPNPFVGTDFENRKH 183
DB 99 KLMKLAQKESARRPFIYEAQVGSNNMLESAAHPGWFICTSCNCPNPFVGTDFENRKH 158
QY 184 IEFSFQPVCKAEMSPSEVSD 203
DB 159 IEFSFQPVCKAEMSPSEVSD 178
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 9, 2004, 13:23:09 ; Search time 48 Seconds

(without alignments)
1356.250 Million cell updates/sec

Title: US-09-869-566-5

Perfect score: 1059

Sequence: 1 MSALLILALYGAADVADYKDD.....IEFSQPVCKAEKSPSEVSD 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320695617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	906	85.6	192	10	US-09-876-790-3
2	906	85.6	192	14	US-10-139-833-13
3	902	85.2	197	10	US-09-876-790-9
4	895	84.5	198	9	US-09-788-963-6
5	895	84.5	218	9	US-09-788-963-2
6	895	84.5	218	10	US-09-876-790-8
7	895	84.5	218	12	US-10-695-195-4
8	895	84.5	218	14	US-10-139-833-12
9	895	84.5	218	14	US-10-302-554-2
10	895	84.5	218	16	US-10-694-978-4
11	895	84.5	218	16	US-10-679-201-6
12	891	84.1	218	14	US-10-302-554-14
13	885	83.6	193	12	US-10-063-745-142
14	885	83.6	193	12	US-10-063-512-142
15	885	83.6	193	12	US-10-063-513-142

16	885	83.6	193	12	US-10-063-515-142
17	885	83.6	193	12	US-10-063-549-142
18	885	83.6	193	12	US-10-063-569-142
19	885	83.6	193	12	US-10-063-551-142
20	885	83.6	193	12	US-10-063-555-142
21	885	83.6	193	12	US-10-063-563-142
22	885	83.6	193	12	US-10-063-594-142
23	885	83.6	193	12	US-10-063-553-142
24	885	83.6	193	12	US-10-063-554-142
25	885	83.6	193	13	US-10-006-867-142
26	885	83.6	193	13	US-10-063-547-142
27	885	83.6	193	14	US-10-063-616-142
28	885	83.6	193	14	US-10-063-502-142
29	885	83.6	193	14	US-10-063-518-142
30	885	83.6	193	14	US-10-063-598-142
31	885	83.6	193	14	US-10-227-693-142
32	885	83.6	193	14	US-10-063-567-142
33	885	83.6	193	14	US-10-063-538-142
34	885	83.6	193	14	US-10-063-599-142
35	885	83.6	193	14	US-10-063-595-142
36	885	83.6	193	14	US-10-063-580-142
37	885	83.6	193	14	US-10-063-557-142
38	885	83.6	193	14	US-10-063-585-142
39	885	83.6	193	14	US-10-063-588-142
40	885	83.6	193	14	US-10-063-735-142
41	885	83.6	193	14	US-10-063-526-142
42	885	83.6	193	14	US-10-063-596-142
43	885	83.6	193	14	US-10-063-546-142
44	885	83.6	193	14	US-10-063-564-142
45	885	83.6	193	14	US-10-063-662-142

ALIGNMENTS

RESULT 1
US-09-876-790-3
Sequence 3, Application US/09876790

Publication No. US20030091532A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPICE VARIANTS AND XREC2 DNAS AND POLYPEPT.
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/09/876,790
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-790-3

Query Match 85.6%; Score 906; DB 10; Length 192;

Best Local Similarity 100.0%; Pred. No. 4.7e-91;

Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 RGPVKVNLNPKFSDHDKVLDGSLNLTAVDPKVIKIRPEIFPALASSISSASAEKGS 92

Db 22 RGPVKVNLNPKFSDHDKVLDGSLNLTAVDPKVIKIRPEIFPALASSISSASAEKGS 81

QY 93 PILLGVSGKEFCLYCDKDGKQSHPSLQKXKXLMKLAQKESARRPFTFYRAQVGSWNML 152

Db 82 PILLGVSGKEFCLYCDKDGKQSHPSLQKXKXLMKLAQKESARRPFTFYRAQVGSWNML 141

QY 153 ESAAHFGWICTSCNCPVGVTDKFNKXKHFSPQVCKAEMSPSEVSD 203
Db 142 ESAAHFGWICTSCNCPVGVTDKFNKXKHFSPQVCKAEMSPSEVSD 192

RESULT 2

US-10-139-833-13

; Sequence 13, Application US/10139833

; Publication No. US20030004106A1

; GENERAL INFORMATION:

; APPLICANT: Saris, Christiaan M.

; APPLICANT: Giles, Jennifer

; APPLICANT: Mu, Sharon X.

; APPLICANT: Xia, Min

; APPLICANT: Bass, Michael B.

; APPLICANT: Cravairo, Roger

; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and

; FILE REFERENCE: 00-1213-E

; CURRENT APPLICATION NUMBER: US/10/139,833

; CURRENT FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: 60/170,191

; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: 60/188,053

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: 60/194,521

; PRIOR FILING DATE: 2000-04-04

; PRIOR APPLICATION NUMBER: 60/195,910

; PRIOR FILING DATE: 2000-04-10

; PRIOR APPLICATION NUMBER: 09/724,583

; PRIOR FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 13

; LENGTH: 192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-139-833-13

Query Match 85.6%; Score 906; DB 14; Length 192;
Best Local Similarity 100.0%; Pred. No. 4,7e-91;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 RGPVKVNLNPKFSDHDKVLDGSLNLIAPVDKNIYRPIFFALASLSAESAEGS 92

Db 22 RGPVKVNLNPKFSDHDKVLDGSLNLIAPVDKNIYRPIFFALASLSAESAEGS 81

QY 93 PILLGVSKGEFCLYCDKQSHPSLQKKEKMLKLAQKESARRPFIFRYAQVGSWNML 152

Db 82 PILLGVSKGEFCLYCDKQSHPSLQKKEKMLKLAQKESARRPFIFRYAQVGSWNML 141

QY 153 ESAAHFGWICTSCNCPVGVTDKFNKXKHFSPQVCKAEMSPSEVSD 203

Db 142 ESAAHFGWICTSCNCPVGVTDKFNKXKHFSPQVCKAEMSPSEVSD 192

RESULT 3

US-09-876-790-9

; Sequence 9, Application US/09876790

; Publication No. US20030091532A1

; GENERAL INFORMATION:

; APPLICANT: SIMS, John E.

; APPLICANT: SMITH, Dirk E.

; APPLICANT: BORN, Teresa L.

; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPICE VARIANTS AND XREC2 DNAS AND POLYPEPTI

; FILE REFERENCE: 2008-US

; CURRENT APPLICATION NUMBER: US/09/876,790

; CURRENT FILING DATE: 2002-09-04

; PRIOR APPLICATION NUMBER: 60/112,163

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: 60/146,675

; PRIOR FILING DATE: 1999-11-10

; PRIOR APPLICATION NUMBER: PCT/US99/29549

; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 9
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-790-9

Query Match 85.2%; Score 902; DB 10; Length 197;
Best Local Similarity 91.5%; Pred. No. 1.4e-90;
Matches 172; Conservative 4; Mismatches 6; Indels 6; Gaps 1;

QY 16 DYKDDDDKLAANSALCRGKVKVNLNPKFSDHDKVLDGSLNLIAPVDKNIYRPI 75

Db 16 DWKDEPQ-----CCLEGPKVNLNPKFSDHDKVLDGSLNLIAPVDKNIYRPI 69

QY 76 FFALASSLSASAEGSPILLGVSKGEFCLYCDKQSHPSLQKKEKMLKLAQKESA 135

Db 70 FFALASSLSASAEGSPILLGVSKGEFCLYCDKQSHPSLQKKEKMLKLAQKESA 129

QY 136 RRPFIYFRAQVGSWNMLESAHPGWICTSCNCPVGVTDKFNKXKHFSPQVCKAE 195

Db 130 RRPFIYFRAQVGSWNMLESAHPGWICTSCNCPVGVTDKFNKXKHFSPQVCKAE 189

QY 196 MSPSEVSD 203

Db 190 MSPSEVSD 197

RESULT 4

US-09-788-963-6

; Sequence 6, Application US/09788963

; Patent No. US20020052473A1

; GENERAL INFORMATION:

; APPLICANT: YOUNG, PETER R.

; APPLICANT: MCDONNELL, PETER C.

; APPLICANT: KUNAR, SANJAY

; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4

; FILE REFERENCE: GP-70607-1C1

; CURRENT APPLICATION NUMBER: US/09/788,963

; CURRENT FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 09/293,625

; PRIOR FILING DATE: 1999-04-16

; PRIOR APPLICATION NUMBER: 09/452,140

; PRIOR FILING DATE: 1999-12-01

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 198

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-788-963-6

Query Match 84.5%; Score 895; DB 9; Length 198;
Best Local Similarity 100.0%; Pred. No. 8e-90;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 PKVKNLNPXKFSIHDQDHKVLVDGSLNLIAPVDKNIYRPIFFALASSLSASAEGSPI 94

Db 30 PKVKNLNPXKFSIHDQDHKVLVDGSLNLIAPVDKNIYRPIFFALASSLSASAEGSPI 89

QY 95 LLGVSKGEFCLYCDKQSHPSLQKKEKMLKLAQKESARRPFIFRYAQVGSWNMLE 154

Db 90 LLGVSKGEFCLYCDKQSHPSLQKKEKMLKLAQKESARRPFIFRYAQVGSWNMLE 149

QY 155 AAHPGWICTSCNCPVGVTDKFNKXKHFSPQVCKAEMSPSEVSD 203

Db 150 AAHPGWICTSCNCPVGVTDKFNKXKHFSPQVCKAEMSPSEVSD 198

RESULT 5

US-09-788-963-2